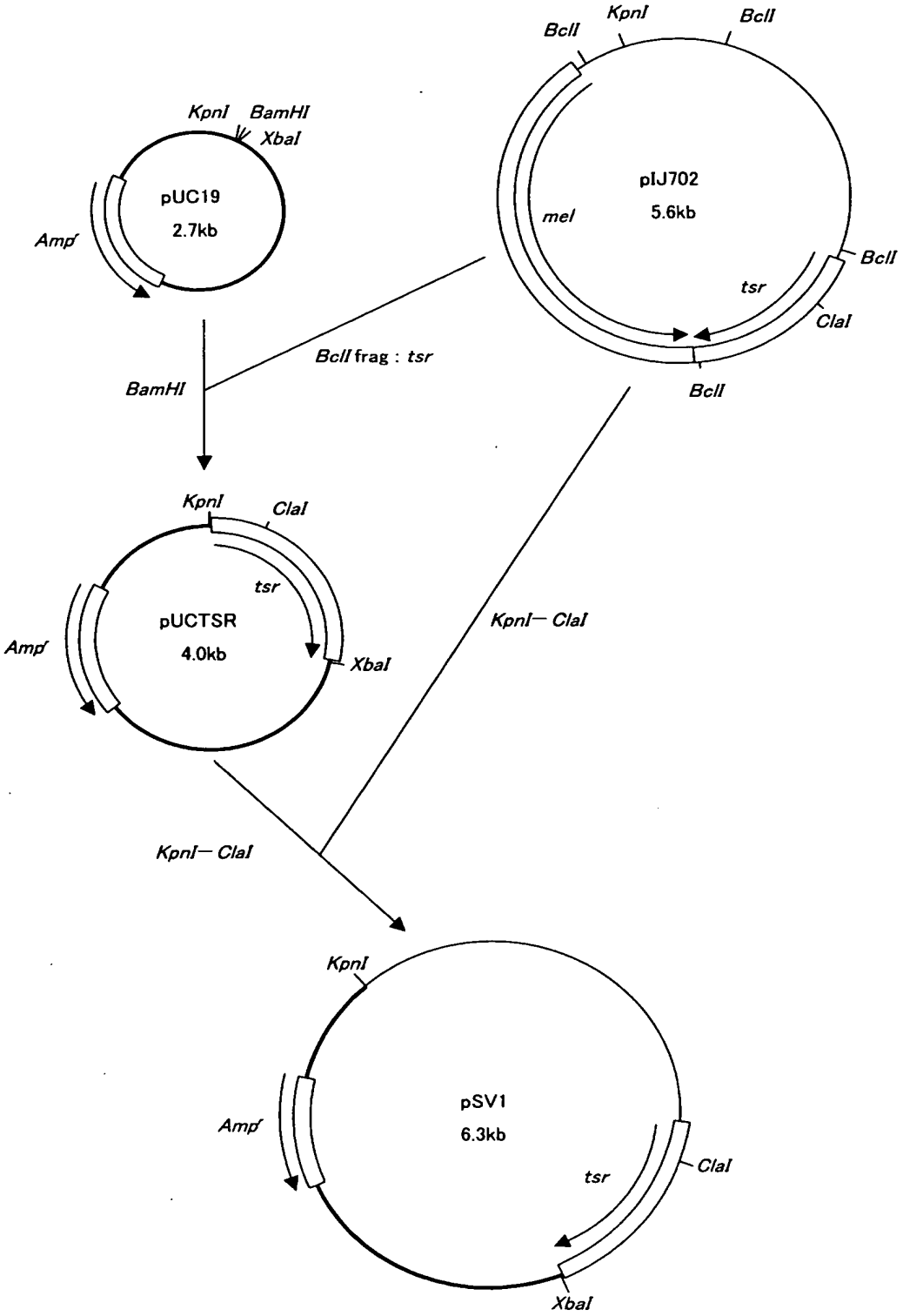
Fig.1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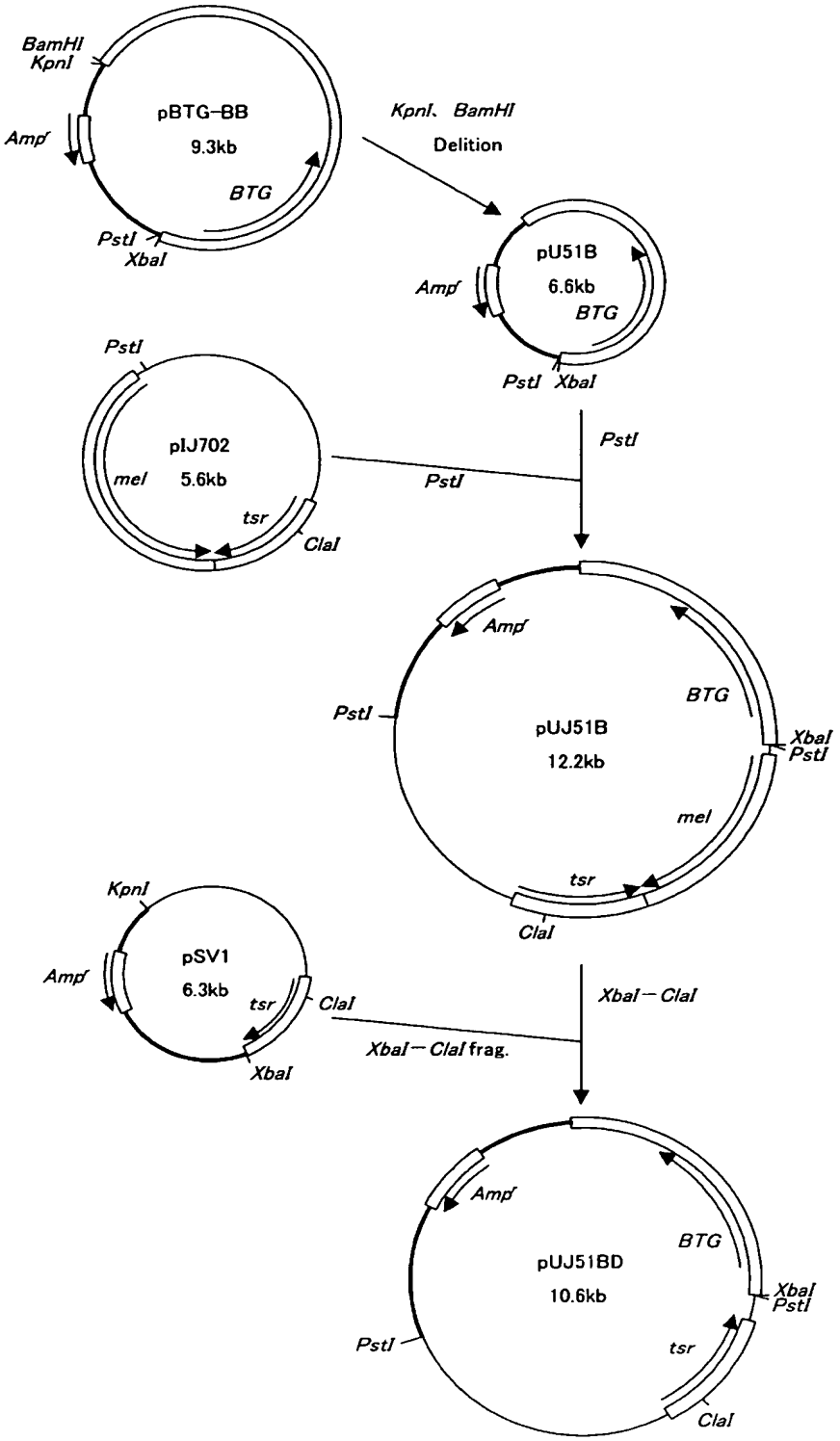
pUC19
2.7kb
Amp
BamHI
BclI frag : tsr
BclI
KpnI
BclI
pIJ702
5.6kb
mel
tsr
BclI
ClaI
BclI
KpnI
ClaI
tsr
pUCTSR
4.0kb
Amp
XbaI
KpnI— ClaI
KpnI— ClaI
KpnI
pSV1
6.3kb
Amp
tsr
ClaI
XbaI

Fig.2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KpnI
pBTG-BB
9.3kb
Amp
BTG
PstI
XbaI
KpnI、BamHI
Delition
pU51B
6.6kb
Amp
BTG
PstI XbaI
PstI
pIJ702
mel
5.6kb
tsr
ClaI
PstI
PstI
Amp
BTG
PstI
pUJ51B
12.2kb
XbaI
PstI
mel
tsr
ClaI
KpnI
pSV1
6.3kb
Amp
tsr
ClaI
XbaI
XbaI－ClaI
XbaI－ClaI frag.
Amp
BTG
pUJ51BD
10.6kb
XbaI
PstI
PstI
tsr
ClaI

Fig.3

Sequence Range: 1 to 669

```
        10         20         30         40         50         60
GATCTTCCGG GACATCTGAG GCGCCGGAGG CGATCCGAGG CGCCCGAGGC GTCTGCGCGA

        70         80         90        100        110        120
AGGGCGCCGC CGTGCCGTCC ATCCCCGTCC GCGTCGACGC GGGCCGGGAG GGGGTGCGGC

       130        140        150        160        170        180
GGCGCCCTTC GGCTGTGTGG ACGAAGCGTC GGGTCGGAGG GGCGGCCGGA TATCGTCCTT

       190        200        210        220        230        240
GGGGCGGGGT GGCCGGAATT GCCGCCATGG TGTTGCCGGG GAATCGACCC GAAGACATGA

       250        260        270        280        290        300
TCACTTCTCG TATCCACCCG ATCACGTATC CGGGAGTCGA GAAGTGTTAC GCCGTGCCCC

       310        320        330        340        350        360
TGTCCGCGTC CTCACCCCTG TCGCCGTGAC AGCGACCCGC GTTCTTCCAC TCGCACGGAC

       370        380        390        400        410        420
GGCCCCACAG GACCTTTCGG CCCGGGCTCG CCCCGCCGCC TCGGTGACGG CCTCCGAATA

       430        440        450        460        470        480
ACGCGGCCGC CGGGGCCTCG GCCGGTTGAC CGATCCGGGT CACGCGCCCC GCCGGGCGGG

       490        500        510        520        530        540
CGGCCACGTC CGGTCTCGCC CCGCCCGACA TCGGCTGCGA CTGCCTTCGC TCGCACTTCT

       550        560        570        580        590        600
TCCCGCCTCC CGGCCGCGTT TTTCCGCCGC CGAAGGTGCG GCGACGCGTA CCGAATCCCC

       610        620        630        640        650        660
CTTCATCGCG ACGTGCTTCC GCACGGCCGC GTTCAACGAT GTTCCACGAC AAAGGAGTTG

CAGGTTTCC
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Fig.4

```
GATCTTCCGG GACATCTGAG GCGCCGGAGG CGATCCGAGG CGCCCGAGGC GTCTGCGCGA 60

AGGGCGCCGC CGTGCCGTCC ATCCCCGTCC GCGTCGACGC GGGCCGGGAG GGGGTGCGGC 120

GGCGCCCTTC GGCTGTGTGG ACGAAGCGTC GGGTCGGAGG GGCGGCCGGA TATCGTCCTT 180

GGGGCGGGGT GGCCGGAATT GCCGCCATGG TGTTGCCGGG GAATCGACCC GAAGACATGA 240

TCACTTCTCG TATCCACCCG ATCACGTATC CGGGAGTCGA GAAGTGTTAC GCCGTGCCCC 300

TGTCCGCGTC CTCACCCCTG TCGCCGTGAC AGCGACCCGC GTTCTTCCAC TCGCACGGAC 360

GGCCCCACAG GACCTTTCGG CCCGGGCTCG CCCCGCCGCC TCGGTGACGG CCTCCGAATA 420

ACGCGGCCGC CGGGGCCTCG GCCGGTTGAC CGATCCGGGT CACGCGCCCC GCCGGGCGGG 480

CGGCCACGTC CGGTCTCGCC CCGCCCGACA TCGGCTGCGA CTGCCTTCGC TCGCACTTCT 540

TCCCGCCTCC CGGCCGCGTT TTTCCGCCGC CGAAGGTGCG GCGACGCGTA CCGAATCCCC 600

CTTCATCGCG ACGTGCTTCC GCACGGCCGC GTTCAACGAT GTTCCACGAC AAAGGAGTTG 660

CAGGTTTCC ATG CGC ATA CGC CGG AGA GCT CTC GTC TTC GCC ACT ATG AGT
          Met Arg Ile Arg Arg Arg Ala Leu Val Phe Ala Thr Met Ser>
            1               5                  10

        720
GCG GTG TTA TGC ACC GCC GGA TTC ATG CCG TCG GCC GGC GAG GCC GCC
Ala Val Leu Cys Thr Ala Gly Phe Met Pro Ser Ala Gly Glu Ala Ala>

                        780
GCC GAC AAT GGC GCG GGG GAA GAG ACG AAG TCC TAC GCC GAA ACC TAC
Ala Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr>

                                            840
CGC CTC ACG GCG GAT GAC GTC GCG AAC ATC AAC GCG CTC AAC GAA AGC
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser>

                                                        900
GCT CCG GCC GCT TCG AGC GCC GGC CCG TCG TTC CGG GCC CCC GAC TCC
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser>

GAC GAC AGG GTC ACC CCT CCC GCC GAG CCG CTC GAC AGG ATG CCC GAC
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp>

        960
CCG TAC CGT CCC TCG TAC GGC AGG GCC GAG ACG GTC GTC AAC AAC TAC
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr>

                        1020
ATA CGC AAG TGG CAG CAG GTC TAC AGC CAC CGC GAC GGC AGG AAG CAG
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln>

                                            1080
CAG ATG ACC GAG GAG CAG CGG GAG TGG CTG TCC TAC GGC TGC GTC GGT
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly>

                                                        1140
GTC ACC TGG GTC AAT TCG GGT CAG TAC CCG ACG AAC AGA CTG GCC TTC
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe>

GCG TCC TTC GAC GAG GAC AGG TTC AAG AAC GAG CTG AAG AAC GGC AGG
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg>

        1200
CCC CGG TCC GGC GAG ACG CGG GCG GAG TTC GAG GGC CGC GTC GCG AAG
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys>

                        1260
GAG AGC TTC GAC GAG GAG AAG GGC TTC CAG CGG GCG CGT GAG GTG GCG
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala>
```

Fig.5

```
                                                    1320
TCC GTC ATG AAC AGG GCC CTG GAG AAC GCC CAC GAC GAG AGC GCT TAC
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr>

                                                              1380
CTC GAC AAC CTC AAG AAG GAA CTG GCG AAC GGC AAC GAC GCC CTG CGC
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg>

AAC GAG GAC GCC CGT TCC CCG TTC TAC TCG GCG CTG CGG AAC ACG CCG
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro>

       1440
TCC TTC AAG GAG CGG AAC GGA GGC AAT CAC GAC CCG TCC AGG ATG AAG
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys>

                          1500
GCC GTC ATC TAC TCG AAG CAC TTC TGG AGC GGC CAG GAC CGG TCG AGT
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser>

                                                    1560
TCG GCC GAC AAG AGG AAG TAC GGC GAC CCG GAC GCC TTC CGC CCC GCC
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala>

                                                              1620
CCG GGC ACC GGC CTG GTC GAC ATG TCG AGG GAC AGG AAC ATT CCG CGC
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg>

AGC CCC ACC AGC CCC GGT GAG GGA TTC GTC AAT TTC GAC TAC GGC TGG
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp>

       1680
TTC GGC GCC CAG ACG GAA GCG GAC GCC GAC AAG ACC GTC TGG ACC CAC
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His>

                          1740
GGA AAT CAC TAT CAC GCG CCC AAT GGC AGC CTG GGT GCC ATG CAT GTC
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val>

                                                    1800
TAC GAG AGC AAG TTC CGC AAC TGG TCC GAG GGT TAC TCG GAC TTC GAC
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp>

                                                              1860
CGC GGA GCC TAT GTG ATC ACC TTC ATC CCC AAG AGC TGG AAC ACC GCC
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala>

CCC GAC AAG GTA AAG CAG GGC TGG CCG TGA TGTGAGC GGGGTGGAGG
Pro Asp Lys Val Lys Gln Gly Trp Pro ***>

                    1920
GGAGCCGGTT GCCCGGCTCC CCTCCACCCT CTCCCCCGCC ACCACGAAAG TCGCTACAGC

                    1980
TCGTGTCCCG TCGTGCTGTC GACGTGCGCC GGGAGTTCGC CCTCGTGGCG GTCGCCCGTC

                    2040
GTCGGGGTGC CCGTGGGTTC GAACATGAGG ATGGAGGCGC CCGGGGAGGA CGGCTTGTGT

                    2100
TCGGTGCCCT TGGGCACCAC GAAGGTGTCG CCCTTGTGCA GGCGCACCGT GTGTTCCGTT

                    2160
CCGTCGGAGT CGCGGAGCGC CACGTCGAAG CGGCCGTCCA GGACGAGGAA GAACTCGTCG

                    2220
GTGTCCTCGT GGACGTGCCA GACGTGCTCG CCTCGGGTGT GGGCGACGCG GACGTCGTAG

                    2280
TCGTTCATGC GGGCGACGAT GCGCGGGCTG TAGACGTCGT CGAAGGAGGC GAGGGCCTTG

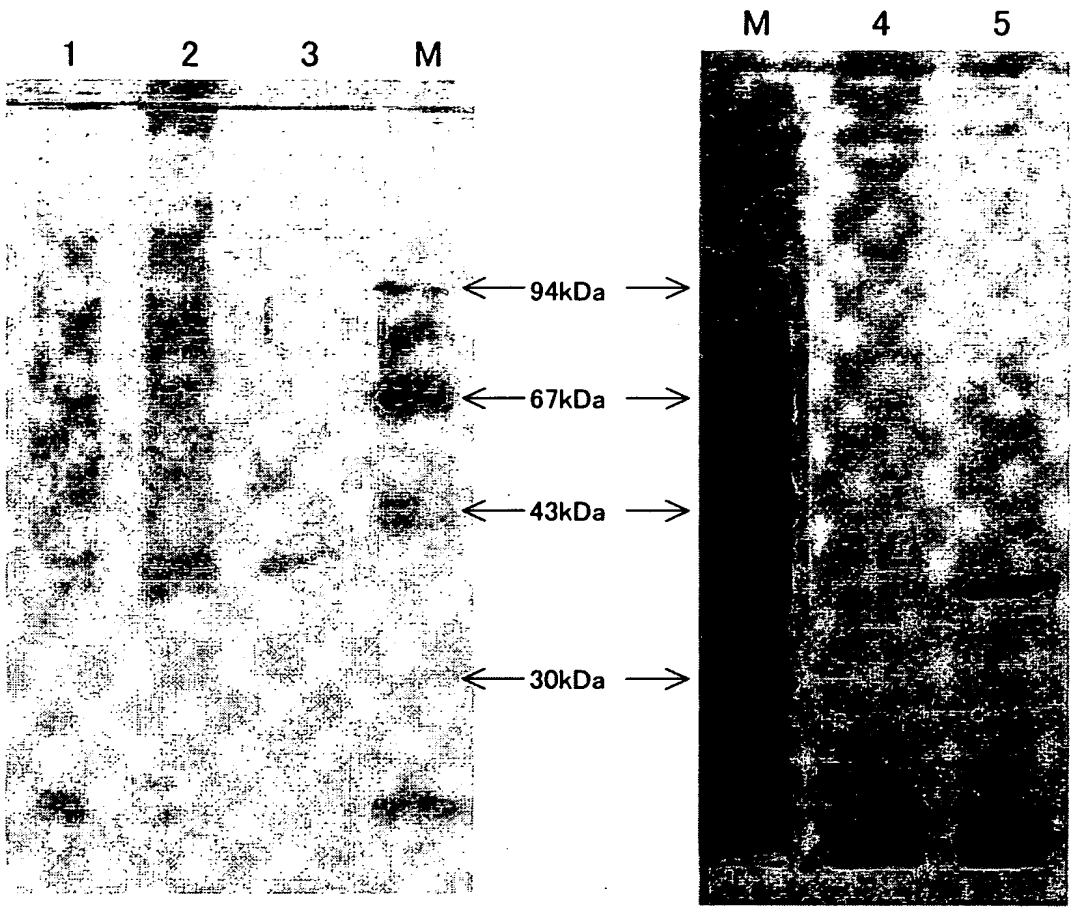
                    2340
GCGAGGTTGA CGGGCTCGGT GTCGTTCATG GTCCGAGTCT CGGCGGGAGC CCGCCGCGGC

GTC
```

Fig.6

	Amount of BTG in culture supernatant
ABL-1 : pUJ51BD／*S.lividans* 3131TS	0.7 g/L
ABM-1 : pUJ51BD／*S.mobaraensis* S-8112	0.5 g/L

Fig.7



1 *S.lividans*

2 ABL-1:pUJ51BD／*S.lividans*

3 Purified BTG

4 *S.mobaraensis*

5 ABM-1:pUJ51BD／*S.mobaraensis*